

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/527,422
Source: IFWP
Date Processed by STIC: 6/9/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 06/09/2006

PATENT APPLICATION: US/10/527,422

TIME: 10:26:49

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06092006\J527422.raw

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3 <110> APPLICANT: BARTOSCH et al.
5 <120> TITLE OF INVENTION: Infectious HCV pseudo-particles containing fonctionnal E1,
E2 envelope
6     proteins
8 <130> FILE REFERENCE: P08575US00/BAS
10 <140> CURRENT APPLICATION NUMBER: US 10/527,422
11 <141> CURRENT FILING DATE: 2005-03-14
13 <150> PRIOR APPLICATION NUMBER: PCT/IB2003/003882
14 <151> PRIOR FILING DATE: 2003-09-12
16 <160> NUMBER OF SEQ ID NOS: 16
18 <170> SOFTWARE: PatentIn version 3.2
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 21
22 <212> TYPE: PRT
23 <213> ORGANISM: Hepatitis C virus : delta C
25 <400> SEQUENCE: 1
27 Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr
28 1           5           10           15
31 Val Pro Ala Ser Ala
32           20
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36 <211> LENGTH: 20
37 <212> TYPE: DNA
38 <213> ORGANISM: Artificial
40 <220> FEATURE:
41 <223> OTHER INFORMATION: primer
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44 actggacgac gcaaagctgc                               20
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48 <211> LENGTH: 29
49 <212> TYPE: DNA
50 <213> ORGANISM: Artificial
52 <220> FEATURE:
53 <223> OTHER INFORMATION: primer
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56 cgcggatcct acgcgtcgac gccggcaaa                     29
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60 <211> LENGTH: 35
61 <212> TYPE: DNA
62 <213> ORGANISM: Artificial
64 <220> FEATURE:
65 <223> OTHER INFORMATION: primer
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91 <400> SEQUENCE: 6
92 tactctgagt ccaaaccg                                18
95 <210> SEQ ID NO: 7
96 <211> LENGTH: 35
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98 <213> ORGANISM: Artificial
100 <220> FEATURE:
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103 <400> SEQUENCE: 7
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118 <222> LOCATION: (1)..(768)
119 <223> OTHER INFORMATION: human cytomegalovirus (hCMV) immediate-early promoter
121 <220> FEATURE:
122 <221> NAME/KEY: misc_feature
123 <222> LOCATION: (769)..(1429)
124 <223> OTHER INFORMATION: rabbit beta-globin intron II
127 <220> FEATURE:
128 <221> NAME/KEY: misc_feature
129 <222> LOCATION: (1425)..(1430)
130 <223> OTHER INFORMATION: BamHI 5'junction after ligation of deltaCE1 fragment in
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131      site of hCMV-G
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136 <223> OTHER INFORMATION: IRES sequence of EMCV
138 <220> FEATURE:
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140 <222> LOCATION: (2116)..(2880)
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 143 <221> NAME/KEY: misc_feature
 144 <222> LOCATION: (2125)..(2304)
 145 <223> OTHER INFORMATION: deltaC part of the polyprotein
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 149 <222> LOCATION: (2305)..(2880)
 150 <223> OTHER INFORMATION: Mature E1 protein
 152 <220> FEATURE:
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 154 <222> LOCATION: (2883)..(2888)
 155 <223> OTHER INFORMATION: BamHI 3' junction after ligation of deltaCE1 fragment in

BamHI

156 site of hCMV-G
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 161 tttatattgg ctcatgtcca acattaccgc catgttgaca ttgattattg actagttatt 120
 163 aatagtaatc aattacgggg tcattagttc atagcccata tatggagttc cgcgttacat 180
 165 aacttacggg aaatggcccc cctggctgac cgcccacga ccccgccca ttgacgtcaa 240
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 171 cccctattga cgtcaatgac ggtaaatggc ccgcctggca ttatgccag tacatgacct 420
 173 tatgggactt tcctacttgg cagtacatct acgtattagt catcgctatt accatggtga 480
 175 tgcggttttg gcagtacatc aatgggcgtg gatagcgggt tgactcacgg ggatttccaa 540
 177 gtctccaccc cattgacgtc aatgggagtt tgttttgga ccaaatcaa cgggactttc 600
 179 caaatgtcg taacaactcc gcccattga cgcaaatggg cggtaggcgt gtacgggtggg 660
 181 aggtctatat aagcagagct cgttttagtga accgtcagat cgctggaga cgccatccac 720
 183 gctgttttga cctccataga agacaccggg accgatccag cctccggtcg accgatcctg 780
 185 agaacttcag ggtgagtttg gggacccttg attgttcttt ctttttcgct attgtaaaat 840
 187 tcatgttata tggagggggc aaagttttca ggggtgttgt tagaatggga agatgtccct 900
 189 tgtatcacca tggaccctca tgataatttt gtttctttca ctttctactc tgttgacaac 960
 191 cattgtctcc tcttattttc ttttcatttt ctgtaacttt ttcgttaaac tttagcttgc 1020
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 195 aatcactttt ttttcaaggc aatcagggtg tattatattg tacttcagca cagttttaga 1140
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 219 ctttgcaggc agcggaaccc ccacctggc gacaggtgcc tctgcggcca aaagccacgt 1860
 221 gtataagata cacctgcaaa ggcggcacia cccagtgcc acgttgtgag ttggatagtt 1920
 223 gtggaaagag tcaaatggct ctctcaagc gtattcaaca aggggctgaa ggatgccag 1980
 225 aaggtagccc attgtatggg atctgatctg gggcctcggt gcacatgctt tacatgtgtt 2040

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227 tagtcgaggt taaaaaacgt ctaggccccc cgaaccacgg ggacgtgggt ttcctttgaa 2100
229 aaacacgata atacc atg aat tcc gac ctc atg ggg tac ata ccg ctc gtc 2151
230           Met Asn Ser Asp Leu Met Gly Tyr Ile Pro Leu Val
231           1           5           10
233 ggc gcc cct ctt gga ggc gct gcc agg gcc ctg gcg cat ggc gtc cgg 2199
234 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg
235           15           20           25
237 gtt ctg gaa gac ggc gtg aac tat gca aca ggg aac ctt cct ggt tgc 2247
238 Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys
239           30           35           40
241 ttt ttc tct atc ttc ctt ctg gcc ctg ctc tct tgc ctg act gtg ccc 2295
242 Phe Phe Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro
243 45           50           55           60
245 gct tca gcc tac caa gtg cgc aat tcc tcg ggg ctt tac cat gtc acc 2343
246 Ala Ser Ala Tyr Gln Val Arg Asn Ser Ser Gly Leu Tyr His Val Thr
247           65           70           75
249 aat gat tgc cct aat tcg agt att gtg tac gag gcg gcc gat gcc atc 2391
250 Asn Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile
251           80           85           90
253 ctg cac act ccg ggg tgt gtc cct tgc gtt cgc gag ggt aac gcc tcg 2439
254 Leu His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser
255           95           100           105
257 agg tgt tgg gtg gcg gtg acc ccc acg gtg gcc acc agg gac ggc aaa 2487
258 Arg Cys Trp Val Ala Val Thr Pro Thr Val Ala Thr Arg Asp Gly Lys
259           110           115           120
261 ctc ccc aca acg cag ctt cga cgt cat atc gat ctg ctt gtc ggg agc 2535
262 Leu Pro Thr Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val Gly Ser
263 125           130           135           140
265 gcc acc ctc tgc tca gcc ctc tac gtg ggg gac ctg tgc ggg tct gtt 2583
266 Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Ser Val
267           145           150           155
269 ttt ctt gtt ggt caa ctg ttt acc ttc tct ccc agg cgc cac tgg acg 2631
270 Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg Arg His Trp Thr
271           160           165           170
273 acg caa agc tgc aat tgt tct atc tat ccc ggc cat ata acg ggt cat 2679
274 Thr Gln Ser Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His
275           175           180           185
277 cgc atg gca tgg gat atg atg aac tgg tcc cct acg gca gcg ttg 2727
278 Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Ala Ala Leu
279           190           195           200
281 gtg gta gct cag ctg ctc cgg atc cca caa gcc atc atg gac atg atc 2775
282 Val Val Ala Gln Leu Leu Arg Ile Pro Gln Ala Ile Met Asp Met Ile
283 205           210           215           220
285 gct ggt gct cac tgg gga gtc ctg gcg ggc ata gcg tat ttc tcc atg 2823
286 Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe Ser Met
287           225           230           235
289 gtg ggg aac tgg gcg aag gtc ctg gta gtg ctg ctg tta ttt gcc ggc 2871
290 Val Gly Asn Trp Ala Lys Val Leu Val Val Leu Leu Leu Phe Ala Gly
291           240           245           250

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293 gtc gac gcg taggatccgt cgaggaattc actcctcagg tgcaggctgc      2920
294 Val Asp Ala
295          255
297 ctatcagaag gtggtggctg gtgtggccaa tgccctggct cacaaatacc actgagatct      2980
299 ttttccctct gccaaaaatt atggggacat catgaagccc cttgagcatc tgacttctgg      3040
301 ctaataaagg aaattttatt tcattgcaat agtgtgttgg aattttttgt gtctctcact      3100
303 cggaaggaca tatgggaggg caaatcattt aaaacatcag aatgagtatt tggtttagag      3160
305 tttggcaaca tatgcccata tgctggctgc catgaacaaa ggttggctat aaagagggtca      3220
307 tcagtatatg aaacagcccc ctgctgtcca ttccttattc catagaaaag ccttgacttg      3280
309 aggttagatt tttttatat tttgttttgt gttatttttt tctttaacat ccctaaaatt      3340
311 ttccttacat gttttactag ccagattttt cctcctctcc tgactactcc cagtcatagc      3400
313 tgtccctctt ctcttatgga gatccctcga cggatcggcc gcaattcgta atcatgtcat      3460
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317 gcataaagtg taaagcctgg ggtgccta at gagtgagcta actcacatta attgcgttgc      3580
319 gctcactgcc cgctttccag tcgggaaacc tgcctgcca gctgcattaa tgaatcggcc      3640
321 aacgcgcggg gagaggcggg ttgctgattg ggcgtcttc cgcttcctcg ctactgact      3700
323 cgctgcgctc ggtcgttcgg ctgcccggag cggtatcagc tcaactcaaag gcggaatac      3760
325 ggttatccac agaatacagg gataacgcag gaaagaacat gtgagcaaaa ggccagcaaa      3820
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345 cttgatccgg caaacaacc accgctggtg gcggtggttt ttttgtttgc aagcagcaga      4420
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349 ctcagtggaa cgaaaactca cgttaaggga ttttggatcat gagattatca aaaaggatct      4540
351 tcacctagat ctttttaaat taaaaatgaa gttttaaatc aatctaaagt atatatgagt      4600
353 aaacttggtc tgacagttac caatgcttaa tcagttaggc acctatctca gcgatctgtc      4660
355 tatttcggtc atccatagtt gcctgactcc ccgtcgtgta gataactacg atacgggagg      4720
357 gcttaccatc tggccccagt gctgcaatga taccgcgaga cccacgctca ccggtccag      4780
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385 aataaacaaa taggggttcc gcgcacattt ccccgaaaag tgccacctaa attgtaagcg      5620
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:2,3,4,5,6,7,8,9,10,11,12,13,14,15

VERIFICATION SUMMARY

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